

Applicant: Katz, et al.  
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In the claims:

Please cancel claims 1-16 without prejudice.

Please cancel claims 19-37 without prejudice.

Please enter the following new claims.

38. (New) A method for determining whether a deletion or insertion of at least 50 base pairs is present in DNA in a test sample comprising the steps of:

- A2
- a) contacting the test sample with amplification reagents, wherein the amplification reagents comprise amplification primers, to form a reaction mixture in which the amplification primers hybridize with a target nucleic acid sequence and a standard nucleic acid sequence in the test sample;
  - b) subjecting the reaction mixture to amplification conditions to form a target nucleic acid sequence amplification product, if the target nucleic acid is present in the test sample, and a standard nucleic acid amplification product;
  - c) detecting a first signal that is proportional to the amount of the target nucleic acid sequence amplification product;
  - d) detecting a second signal that is proportional to the amount of the standard nucleic acid amplification product;
  - e) comparing the first signal to the second signal to determine whether a deletion or insertion of at least 50 base pairs is present in the DNA in the test sample.

39. (new) The method of claim 38 wherein the deletion or insertion is of at least 200 base pairs.

40. (new) The method of claim 38 wherein the deletion or insertion is of at least 1000 base pairs.

41. (new) The method of claim 38 using the amplification conditions of claim 17.